AI FOR GENOMIC AGRICULTURE — FROM SEQUENCE TO FIELD IMPACT

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ABSTRACT

Genomics offers powerful opportunities to enhance crop yield, resilience, and nutritional value, yet the complexity and scale of genomic, transcriptomic, and epigenomic data pose significant challenges for interpretation and application. Artificial intelligence (AI), particularly machine learning and deep learning, provides powerful approaches to decode this complexity and accelerate precision agriculture.

I will present AI-based methods developed in my laboratory for annotating plant and animal genomes, identifying functional genomic regions and predicting the effects of genetic variants. Emerging foundation models for biological sequences, such as ESM-2 and Evo 2, learn rich representations directly from large sequence datasets, offering improved accuracy in linking genetic variants to important agronomic traits. New genome-scale AI systems such as DeepMind's AlphaGenome further extend these capabilities, with potential applications to non-human species, enabling predictive genomics for crops and pests.

I will also highlight real-world applications, including transcriptome analysis of oriental fruit flies to investigate the molecular basis of drug resistance, and genome/transcriptome studies of mungbean to identify genetic factors for bruchid resistance. These AI-driven approaches can guide targeted breeding, enhance stress tolerance, and shorten development cycles, ultimately contributing to sustainable, data-driven agriculture and global food security.

Keywords: Genomic Agriculture, Artificial Intelligence, Foundation Models, Variant Effect Prediction, Precision Trait Development